

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/560,605  
Source: IFWP  
Date Processed by STIC: 9/8/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/560,605

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4      Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length     Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences  
    (OLD RULES)     Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
                               (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               (i)     SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                               (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               This sequence is intentionally skipped  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)     Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                               <210> sequence id number  
                               <400> sequence id number  
                               000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                               Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                               In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10 ✓ Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
  
- 11      Use of <220>     Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
  
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa     "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

DATE: 09/08/2006

PATENT APPLICATION: US/10/560,605

TIME: 13:36:44

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09082006\J560605.raw

5 <110> APPLICANT: Indian Council of Medical Research  
 7 University of Delhi  
 11 <120> TITLE OF INVENTION: Mutants of Mycobacteria and process thereof  
 15 <130> FILE REFERENCE: 11378.0066USWO  
 17 <140> CURRENT APPLICATION NUMBER: US 10/560,605  
 18 <141> CURRENT FILING DATE: 2005-12-13  
 20 <150> PRIOR APPLICATION NUMBER: PCT/IN2004/000203  
 21 <151> PRIOR FILING DATE: 2004-07-09  
 24 <150> PRIOR APPLICATION NUMBER: IP882/DEL/2003  
 25 <151> PRIOR FILING DATE: 2003-07-09  
 29 <160> NUMBER OF SEQ ID NOS: 16  
 33 <170> SOFTWARE: PatentIn version 3.1  
 37 <210> SEQ ID NO: 1  
 39 <211> LENGTH: 32  
 41 <212> TYPE: DNA  
 43 <213> ORGANISM: Artificial Sequence  
 47 <220> FEATURE:  
 49 <223> OTHER INFORMATION: The primer was synthesized  
 51 <400> SEQUENCE: 1  
 52 ccatcatgac gtcgtctgac aacggagcgt cc 32  
 55 <210> SEQ ID NO: 2  
 57 <211> LENGTH: 32  
 59 <212> TYPE: DNA  
 61 <213> ORGANISM: Synthesized  
 65 <400> SEQUENCE: 2  
 66 gggcatatgg caacaccccg gccgcccgt cg 32  
 69 <210> SEQ ID NO: 3  
 71 <211> LENGTH: 33  
 73 <212> TYPE: DNA  
 75 <213> ORGANISM: Synthesized  
 79 <400> SEQUENCE: 3  
 80 gggcatatga cgctcggctg ttgcggcagc tcg 33  
 83 <210> SEQ ID NO: 4  
 85 <211> LENGTH: 32  
 87 <212> TYPE: DNA  
 89 <213> ORGANISM: Synthesized  
 93 <400> SEQUENCE: 4  
 94 ccatcatgac ggtggctggc cccgcggtgc gg 32  
 97 <210> SEQ ID NO: 5  
 99 <211> LENGTH: 33  
 101 <212> TYPE: DNA  
 103 <213> ORGANISM: Synthesized  
 107 <400> SEQUENCE: 5

see pp 1-2  
 Does Not Comply  
 Corrected Diskette Needed

invalid <213> response  
 (see item 10 on Error Summary Sheet)

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Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09082006\J560605.raw

```

108 ccatcatgac tgtggaacct attcctgtcg gcc 33
111 <210> SEQ ID NO: 6
113 <211> LENGTH: 36
115 <212> TYPE: DNA
117 <213> ORGANISM: Synthesized
121 <400> SEQUENCE: 6
122 gggcatatgg gctggattcg cgggctattc ctgtcg 36
125 <210> SEQ ID NO: 7
127 <211> LENGTH: 33
129 <212> TYPE: DNA
131 <213> ORGANISM: Synthesized
135 <400> SEQUENCE: 7
136 gggcatatgg gtgctcacc actgcttcgc ggg 33
139 <210> SEQ ID NO: 8
141 <211> LENGTH: 33
143 <212> TYPE: DNA
145 <213> ORGANISM: Synthesized
149 <400> SEQUENCE: 8
150 ccatcatgag tcggtgaccc cggatatgcc cgg 33
153 <210> SEQ ID NO: 9
155 <211> LENGTH: 28
157 <212> TYPE: DNA
159 <213> ORGANISM: Synthesized
163 <400> SEQUENCE: 9
164 ggcataatggc tgtccgtgaa ctgccggc 28
167 <210> SEQ ID NO: 10
169 <211> LENGTH: 35
171 <212> TYPE: DNA
173 <213> ORGANISM: Synthesized
177 <400> SEQUENCE: 10
178 ggacgcgttc atccgagcag cccccgcgc atccg 35
181 <210> SEQ ID NO: 11
183 <211> LENGTH: 492
185 <212> TYPE: DNA
187 <213> ORGANISM: Mycobacterium tuberculosis
191 <400> SEQUENCE: 11
192 gtgtctgac cgctgcacgt cacattcggt tgtacgggca acatctgccg gtcgccaatg 60
194 gccgagaaga tggtcgccca acagcttcgc caccgtggcc tgggtgacgc ggtgcgagtg 120
196 accagtgcgg gcaccgggaa ctggcatgta ggcagttgcg ccgacgagcg ggcggccggg 180
198 gtgttgcgag ccacaggcta ccctaccgac caccgggccc cacaagtcgg caccgaacac 240
200 ctggcggcag acctgttggt ggccttggac cgcaaccacg ctcggtgtt gcggcagctc 300
202 ggcgtcgaag ccgcccgggt acggatgctg cggtcattcg acccacgctc gggaacccat 360
204 gcgctcgatg tcgaggatcc ctactatggc gatcactccg acttcgagga ggtcttcgcc 420
206 gtcatcgaat ccgccctgcc cggcctgcac gactgggtcg acgaacgtct cgcgcggaac 480
208 ggaccgagtt ga 492
211 <210> SEQ ID NO: 12
213 <211> LENGTH: 831
215 <212> TYPE: DNA
217 <213> ORGANISM: Mycobacterium tuberculosis

```

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Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09082006\J560605.raw

## 221 &lt;400&gt; SEQUENCE: 12

```

222 tcatccgagc agcaccgccg gcacccgggt gactgtggcc tggctgatac cggcgtcgcg      60
224 caggtagccg cccagcgatc cgtaggtctc gtcaatggtc tggcgtcgcg cggccaggta      120
226 ctccgcgcgg acaccagga ccccgctcga cagccgggccc ttggtgaacg tcaccacctc      180
228 ggggtgccagt tcggtgtcga aacgctgctg gatcatctcg gagatccggg cccgcagttg      240
230 tggcacggag tcgttgctgc gcaggtagtc ggcgacgatg acgtcgcggt ccaggccgac      300
232 cgtttcaagc accagcgcca ccacgaagcc ggtgcgatcc ttaccgcgca agcagtgggt      360
234 gagcaccggg cgtccggcgg caagcagtggt gacgacacga tgtagcgcg cgtgtgctcc      420
236 attgcgcggt gggaattggc gatactcgtc ggtcatgtag cgggtggccg cgtcatttat      480
238 cgactggctg gattcgccgg actcgccggt ggaccgcgta ttggttagca gcctcttgaa      540
240 tgcggtttcg tgcggcgctg agtcgctcgg gtcatcatcg gcgaggtcgg ggaacggcag      600
242 caggtggacg tcgatgccgt ccggaacccg tcttgaccg cggcgggcaa cctcccggga      660
244 cgaccgcagg tcggcaacgt cgggtgatccc cagccggcgc agcgttgccc ggccggcgct      720
246 gtcgagggcg ctacgctcgc tggaccggaa cagccggccc ggccgcaatg cggttgcggt      780
248 gtcggcgacg tcacgaaagt tccacgcgcc cggcagttca cggacagcca t          831

```

## 251 &lt;210&gt; SEQ ID NO: 13

## 253 &lt;211&gt; LENGTH: 2531

## 255 &lt;212&gt; TYPE: DNA

## 257 &lt;213&gt; ORGANISM: Mycobacterium tuberculosis

## 261 &lt;400&gt; SEQUENCE: 13

```

262 cgtcgtctga caacggagcg tccaaatcgt cgggcacgcg gtacacgcca tgggtcaatgc      60
264 ctaaccgccc agtctcatga ggatgcagcg gcacaagctt tgctaccggc tcgccgcggc      120
266 gggcaatctc aacctctgcc cgccgtagac gagccgcagc agctcggaca ggcgtgtctt      180
268 cgctcgtga acgccgaccc gcttcgcagg cgcccagact ttccgctcga ccacctgctc      240
270 accaaaactt cgcgatcatcg cctgatacca cagcgccaac gggtagcggt ttgtccaacc      300
272 gcttcgtcaa cgacaatggg atcgtgaccg acacgaccgc gagcgggacc aattgcccgc      360
274 ctctccacg cgccgcgcga cggcgcgcat cgtcgccggg tgaatcgccg cagctggtga      420
276 tcttcgatct ggacggcacg ctgaccgact cggcgcgcgg aatcgatatc agcttcgcag      480
278 acgcgctcaa ccacatcggt gccccagtag ccgaaggcga cctggccact cacatcgctg      540
280 gccgcgccat gcattgagac ctgcgcgcca tggggctcgg cgaatccgcc gagggaggcg      600
282 tcgtagccta ccggggccgac tacagcggccc gcggttgggg gatgaacagc ttgttcgacg      660
284 ggatcggggc gctgctggcc gacctgcgca ccgcccgtgt ccggctggcc gtcgccacct      720
286 ccaaggcaga gccgaccgca cggcgaatcc tgcgccactt cgggaattgag cagcacttcg      780
288 aggtcatcgc gggcgcgagc accgatggct cgcgaggcag caaggctgac gtgctggccc      840
290 acgcgctcgc gcagctgcgg ccgctacccg agcggttggt gatggtcggc gaccgcagcc      900
292 acgacgtcga cggggcgggc gcgcacggca tcgacacggt ggtggtcggc tggggctacg      960
294 ggcgcgccga ctttatcgac aagacctcca ccaccgtcg gacgcatgcc gccacgattg      1020
296 acgagctgag ggaggcgcta ggtgtctgat ccgctgcacg tcacattcgt ttgtacgggc      1080
298 aacatctgcc ggtcgccaat ggccgagaag atgttcgccc aacagcttcg ccaccgtggc      1140
300 ctgggtgacg cggtgcgagt gaccagtgcg ggcaccggga actggcatgt aggcagttgc      1200
302 gccgacgagc gggcgggcgg ggtgttgcca gccacggct acgctcggct gttgcggcag      1260
304 ctcggcgtcg aagccgcccg ggtacggatg ctgcggtcat tcgaccacg ctcgggaacc      1320
306 catgcgctcg atgtcgagga tccctactat ggcgatcact ccgacttcga ggaggtcttc      1380
308 gccgtcatcg aatccgcctt gcccgccctg cacgactggg tcgacgaacg tctcgcgcg      1440
310 aacggaccga gttgatgccc cgcctagcgt tctgtctcgg gcccggtggt ctggcggtgg      1500
312 ccctggtcgt ggtcgcgctt acctacgtg gctttacggt gctcgcgccg tggcagctgg      1560
314 gcaagaatgc caaaacgtca cgagagaacc agcagatcag gtattccctc gacacccgcg      1620
316 cggttccgct gaaaaccctt ctaccacagc aggatctgct gcgcgccggc gcgagtggt      1680
318 gccgggtgac ggcaaccgga cagtaccttc cggacgtgca ggtgctggcc cgactgcgcg      1740

```

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```

320 tgggtggaggg ggaccaggcg tttgaggtgt tggccccatt cgtggtcgac ggcggaccaa 1800
322 ccgtcctggt cgaccgtgga tacgtgcggc cccagggtggg ctgcacgta ccaccgatcc 1860
324 cccgcctgcc ggtgcagacg gtgaccatca ccgcgcggct gcgtgactcc gaaccgagcg 1920
326 tggcggggcaa agaccattc gtcagagacg gcttccagca ggtgtattcg atcaataccg 1980
328 gacaggtcgc cgcgctgacc ggagtccagc tggctgggtc ctatctgcag ttgatcgaag 2040
330 accaaccggy cgggctcggc gtgctcggcg ttccgcattct agatcccggg ccgttccctgt 2100
332 cctatggcat ccaatggatc tggttcggca ttctggcacc gatcggcttg ggctatttctg 2160
334 cctacgccga gatccggggcg cgcgcggggg aaaaagcggg gtcgccacca ccggacaagc 2220
336 caatgacggt cgagcagaaa ctgcgtgacc gctacggccg ccggcggtaa accaacatca 2280
338 cggccaatac cgcagccccc gcctggacca cccgcgacag caccacggcg cggcgagat 2340
340 cggccacctt gggcgaccgg ccgtcgccca aggtggggcg gatctgcaac tcatggtggt 2400
342 accgggtggg cccaccagc cgcacgtcaa gcgcccagc aaacgcccgc tcgacgacac 2460
344 cggcgttggg gctgggatgg cgggcggcgt cgcgcggcca ggcccgtacc gcaccgcggy 2520
346 gcgaccacc g
349 <210> SEQ ID NO: 14
351 <211> LENGTH: 2890
353 <212> TYPE: DNA
355 <213> ORGANISM: Mycobacterium tuberculosis
359 <400> SEQUENCE: 14
360 gtcggtgacc cccgtatagc ccggcgacgt cggtaattta gtagcgccct cgacctgcgc 60
362 gggcgtgagg tccaaatact tgggtgtgtac gaatgtgatg cctgcaaccg cgttgaggtc 120
364 ggaaatgaag ttgagcgggt atcgcgagaa gtccgcgaac ccgtcgtact cgagcgtgta 180
366 gatggccgtc ggatagatcg tgtccgaggg cgttgcgcca tagaacgtca ggtccagagt 240
368 cggaagcgtc agatccggga accgcgcgag cataccgcca ttggggttca ttctattgcc 300
370 gacaagcacg aaattgaggt cgctcgccga aggtgcggcc ccgccatcg ccgtgaacct 360
372 ctgcatctcc agcgacgcga ttatggcgct ttgcgaccag ccgaaaacgg tgaccgcgtt 420
374 tccggtggtc gcgagctcta ccatgatcgc gtcgtgcaag atggtcaagc cctcttccac 480
376 tgacgtgttg aggacaaac ttctgacacc ggtgagtggg tacaactctt cgggtgtgaa 540
378 gacggcttgt agcggccgca gaacggacct acagcgtatt ggcggcgtca acatagacgg 600
380 cgggtgtagt ggaattccgg tgggcccata gaacaagggt gtcaagttcg ccgggaatgg 660
382 cgggaatcatc cgggcccggc cgggggttgg tgcggcgccg ggcacagcca gctgattttg 720
384 cgggtgctg gcgatggcgg cctcggcatc tgcgtagctg ttccgcgcgg cggccaacgt 780
386 ctggtggaac ctaactgtga aacgcctcga cttgagcgag cacggcctgg tattcctggc 840
388 cgtatgcgcc gaacggtttc gcgatggcgg ccgacacctc atcgccggcc gcccgggcca 900
390 gtgcacacgt cgggcctgcc gcggccgcgc cggccgtact cacggccgaa ccgattcctg 960
392 ccacctcgcc ggcggccgcc gctacgatcc gcggctcagc gatcagatac gacatcgtct 1020
394 cactccccta gcaccaggtg tcggccaacc ggtcaaccc ggggttttgg tcagcccaga 1080
396 gcggtcccgc tgccctggtg gtcgcttacg cgaatcggat tcgcgcgaaa gcgtttcccc 1140
398 tcatccgagc agcaccggcg gcacccggtt gactgtggcc tggctgatac cggcgtcgcg 1200
400 caggtagccg cccagcgatc cgtaggtctc gtcaatggtc tggcgtgcgg cggccaggta 1260
402 ctccgcgcgg acaccagga ccccgctcga cagccggggc ttggtgaacg tcaccacctc 1320
404 ggggtgccagt tcggtgtcga aacgctgctg gatcatctcg gagatccggg cccgcagttg 1380
406 tggcacggag tcgttgtcgc gcaggtatgc ggcgacgatg acgtcgcggt ccaggccgac 1440
408 cgcttcaagc accagcgca ccacgaagcc ggtgcgatcc ttaccgcga agcagtgggg 1500
410 gctggattcg ccggactcgc cgttggacct gtcattgggt agcagcctct tgaatgcggt 1560
412 ttcgtgcggc gctgagtcgt cggcgtcatc atcgcgagg tcgggaaacg gcagcaggtg 1620
414 gacgtcgatg acgtccggaa cccgtcctgg accgcggcgg gcaacctccc gggacgacgg 1680
416 caggtcggca agctcggtag tccccagccg gcgcagcgtt gcccgccggc cgtcgtcgag 1740
418 gcggctcagc tcgctggacc ggaacagccg ccccgccgcg aatgcggttg cgggtgcggc 1800

```

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TIME: 13:36:44

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09082006\J560605.raw

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420 gacgtcacga aagttccacg cgcccggcag ttcacggaca gccatctcag gtgaccgccg 1860
422 cagcgaaggt ggactttctcc ctgcacagct cggcgcgggc gatggagcgc aggtgcacct 1920
424 cgtcgggacc gtcgaagatg cgcattggcg ggtgccagcc gtacaaccgg gccagcgggg 1980
426 tgtcgtcgct gacgccggcg gcccctgga cctggattgc gcggtcgatg acatcgcagg 2040
428 ccacccgcgg ggccaccgcc ttgatcatgg cgaccagggtg gcgcgcctct ttgttgccat 2100
430 gttgtcgat tgtccacgcc gctttttcgc acagcagcct tgccctggcg atttcgttgc 2160
432 gggactgagc aatcgctgt tgacagacgc cctgttcggc tagcggagcg ccgaacgcc 2220
434 cccggttgcg gacgcgattc accatgagtg ccaaggcgcg ttcggccgcg cccagcgcac 2280
436 gcatgcagtg gtggatacgg cccggcccca gccgggcctg ggctatggcg aatccgctgc 2340
438 cctcttcgcc gagcagggtg gtggccggga cccggacgtt gtggtagtcg atctcgagtg 2400
440 ggccgtgccg gtcctgccag ccgaacaccg gtgtggagcg aacgatcgtc acgccggggg 2460
442 tgtcgatcgg gacgaggacc atcgactgct gttggtgggc ggctgcgtcc gggttggtgc 2520
444 ggcccatcac gatgaggatc ttgcaccgcg ggtccgcgcg tcccgcagtc caccattac 2580
446 ggccgttgat gacgtagtcg gcacgtccc gggagatggg ggtttcgatg ttgcgggcgt 2640
448 cgctgctggc caccgcggcg tcggtcatcg agaaggcgct gcggatcttg ccgtcgagca 2700
450 cgggccgcag ccattgcgcc cgttgcgtgc cgttgccgaa catgtgcagg atctccatgt 2760
452 tgccggtgtc cgttgccggc cagttgagtg cctcgggcg cgtttccatg ctccatccgg 2820
454 tcatttcggc cagcggcgcg tactccaggt tggtaaatcc cgactcggcc gacaggaata 2880
456 ggttccaag 2890
459 <210> SEQ ID NO: 15
461 <211> LENGTH: 4163
463 <212> TYPE: DNA
465 <213> ORGANISM: Artificial sequence
469 <220> FEATURE:
471 <223> OTHER INFORMATION: The sequence was produced in the lab
473 <400> SEQUENCE: 15
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476 ctaaccgccg agtctcatga ggatgcagcg gcacaagctt tgctaccggc tcgccgcggc 120
478 gggcaatctc aacctctgcc cgccgtagac gagccgcagc agctcggaca ggcgtgtctt 180
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**VERIFICATION SUMMARY**

DATE: 09/08/2006

PATENT APPLICATION: US/10/560,605

TIME: 13:36:45

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\09082006\J560605.raw